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RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/813,323B

DATE: 06/27/2002

TIME: 13:04:49

Input Set : A:\50659.txt

Output Set: N:\CRF3\06272002\H813323B.raw

3 <110> APPLICANT: Baltimore, David
 4 Cheng, Genhong
 5 Ye, Zheng-Sheng
 6 Lederman, Seth
 7 Cleary, Aileen
 9 <120> TITLE OF INVENTION: Truncated Craf-1 Inhibits CD40 Signalling
 11 <130> FILE REFERENCE: 0575/50659
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/08/813,323B
 C--> 14 <141> CURRENT FILING DATE: 2002-06-17
 16 <160> NUMBER OF SEQ ID NOS: 5
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 567
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Mouse Sp.
 25 <400> SEQUENCE: 1
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 28 1 5 10 15
 31 Pro Pro Leu Lys Leu Gln Pro Asp Arg Gly Ala Gly Ser Val Leu Val
 32 20 25 30
 35 Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu Asp
 36 35 40 45
 39 Lys Tyr Lys Cys Glu Lys Cys Arg Leu Val Leu Cys Asn Pro Lys Gln
 40 50 55 60
 43 Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu Leu
 44 65 70 75 80
 47 Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Ile Lys
 48 85 90 95
 51 Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala Leu
 52 100 105 110
 55 Gln Val Tyr Cys Arg Asn Glu Gly Arg Gly Cys Ala Glu Gln Leu Thr
 56 115 120 125
 59 Leu Gly His Leu Leu Val His Leu Lys Asn Glu Cys Gln Phe Glu Glu
 60 130 135 140
 63 Leu Pro Cys Leu Arg Ala Asp Cys Lys Glu Lys Val Leu Arg Lys Asp
 64 145 150 155 160
 67 Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys
 68 165 170 175
 71 Ser His Cys Lys Ser Gln Val Pro Met Ile Lys Leu Gln Lys His Glu
 72 180 185 190
 75 Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser
 76 195 200 205
 79 Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys

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| | | | |
|-----|---|-----|-----|
| 80 | 210 | 215 | 220 |
| 83 | Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe | | |
| 84 | 225 | 230 | 235 |
| 87 | Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val | | 240 |
| 88 | 245 | 250 | 255 |
| 91 | Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys | | |
| 92 | 260 | 265 | 270 |
| 95 | Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln | | |
| 96 | 275 | 280 | 285 |
| 99 | Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln | | |
| 100 | 290 | 295 | 300 |
| 103 | Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg | | |
| 104 | 305 | 310 | 315 |
| 107 | Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile | | 320 |
| 108 | 325 | 330 | 335 |
| 111 | Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser | | |
| 112 | 340 | 345 | 350 |
| 115 | Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys | | |
| 116 | 355 | 360 | 365 |
| 119 | Ser Ala Gly Gln Ala Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu | | |
| 120 | 370 | 375 | 380 |
| 123 | Ser Arg His Asp Gln Thr Leu Ser Val His Asp Ile Arg Leu Ala Asp | | |
| 124 | 385 | 390 | 395 |
| 127 | Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val | | |
| 128 | 405 | 410 | 415 |
| 131 | Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val | | |
| 132 | 420 | 425 | 430 |
| 135 | Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr | | |
| 136 | 435 | 440 | 445 |
| 139 | Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met | | |
| 140 | 450 | 455 | 460 |
| 143 | Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu | | |
| 144 | 465 | 470 | 475 |
| 147 | Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met | | 480 |
| 148 | 485 | 490 | 495 |
| 151 | Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys | | |
| 152 | 500 | 505 | 510 |
| 155 | Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn | | |
| 156 | 515 | 520 | 525 |
| 159 | Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn | | |
| 160 | 530 | 535 | 540 |
| 163 | Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp | | |
| 164 | 545 | 550 | 555 |
| 167 | Thr Ser Asp Leu Pro Asp Pro | | 560 |
| 168 | 565 | | |
| 171 | <210> SEQ ID NO: 2 | | |
| 172 | <211> LENGTH: 568 | | |
| 173 | <212> TYPE: PRT | | |
| 174 | <213> ORGANISM: Homo Sapiens | | |

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176 <400> SEQUENCE: 2
 178 Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
 179 1 5 10 15
 182 Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
 183 20 25 30
 186 Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
 187 35 40 45
 190 Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
 191 50 55 60
 194 Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
 195 65 70 75 80
 198 Leu Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
 199 85 90 95
 202 Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
 203 100 105 110
 206 Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
 207 115 120 125
 210 Thr Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu
 211 130 135 140
 214 Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys
 215 145 150 155 160
 218 Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr
 219 165 170 175
 222 Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His
 223 180 185 190
 226 Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys
 227 195 200 205
 230 Ser Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu
 231 210 215 220
 234 Cys Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val
 235 225 230 235 240
 238 Phe Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala
 239 245 250 255
 242 Val Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys
 243 260 265 270
 246 Lys Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile
 247 275 280 285
 250 Gln Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg
 251 290 295 300
 254 Gln Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln
 255 305 310 315 320
 258 Arg Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu
 259 325 330 335
 262 Ile Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser
 263 340 345 350
 266 Ser Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp
 267 355 360 365
 270 Lys Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln
 271 370 375 380

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274 Leu Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala
275 385 390 395 400
278 Asp Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly
279 405 410 415
282 Val Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala
283 420 425 430
286 Val Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly
287 435 440 445
290 Tyr Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly
291 450 455 460
294 Met Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly
295 465 470 475 480
298 Glu Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu
299 485 490 495
302 Met Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe
303 500 505 510
306 Lys Pro Asp Pro Asn Ser Ser Phe Lys Lys Pro Thr Gly Glu Met
307 515 520 525
310 Asn Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu
311 530 535 540
314 Asn Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val
315 545 550 555 560
318 Asp Thr Ser Asp Leu Pro Asp Pro
319 565
322 <210> SEQ ID NO: 3
323 <211> LENGTH: 2359
324 <212> TYPE: DNA
325 <213> ORGANISM: Mouse Sp.
327 <400> SEQUENCE: 3
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330 tccccattac ttgaaggata aggctggcac ggctccgacg tctgtgtgga agtttctccc 120
332 tcccttctga gcttcctctag actccttaca ggcacacggca cagaatttca gtttcctaag 180
334 atggagtcaa gcaaaaagat ggatgtctgt ggcacactgc agcctaacc acccctaaag 240
336 ctgcagccctg atcgcggcgc agggtccgtg ctcgtgccgg agcaaggagg ctacaaggag 300
338 aagtttgtga agacggtgga agacaagtac aagtgcgaga agtgcgcct ggtgtgtgc 360
340 aacccgaagc agacggagtg tggccacccgg ttctgcgaga gctgcattgc cgcctgtcg 420
342 agtccttcca gtccaaaatg cacagcgtgc caagaaagca tcatcaaaga caaggtgttt 480
344 aaggataatt gctcaagag agagattctg gcccattcagg tctactgtcg gaatgaaggc 540
346 agaggttgcg cggagcagct gactctggga catctgtgg tgcaccta aaatgaatgt 600
348 cagtttgagg aactttccctg tctgcgtgcc gactgcaaag aaaaagtact gagaaaagac 660
350 ttgcgggatc acgtgaaaaa ggcctgtaaa taccgcgagg ccacgtgcag tcactgcaag 720
352 agccaagtgc ccatgatcaa actgcagaaa catgaagaca cagattgtcc ctgtgtgg 780
354 gtatcctgcc ctcacaagtgc cagcgttcag actcttctaa ggagttagttt gagatcgac 840
356 ttgtcccgagt gtgtcaatgc cccagcacc tttttt agcgttatgg ctgcgttttt 900
358 cagggtacaa accagcagat caaggcccat gaggccagct ccgcggtaa gcacgtgaac 960
360 ctgctgaagg agtggagcaa ctccctggag aagaaggttt ccctgtgtca gaatgaaagt 1020
362 gttgagaaaa acaagagcat ccaaagcctg cacaaccaga tctgcagctt tgagatcgag 1080
364 attgagaggc agaaggagat gctccgaaac aacgagtcca agatccttca cctgcagcgg 1140
366 gtaatcgaca gccaagcaga gaaactgaaa gaactggaca aggagatccg tcccttccgg 1200

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| | | | | | | | |
|-----|--------------|-------------|--------------|-------------|-------------|--------------|------|
| 368 | cagaactggg | aggaagcgg | cagcatgaag | agcagtgtgg | agtccctcca | gaaccgagtg | 1260 |
| 370 | actgagctgg | agagcgtaga | caaaagtgcg | gggcaggcgg | ctcgcaacac | aggcttgctg | 1320 |
| 372 | gagtcccagc | tgagccggca | tgaccagacg | ttgagtggtc | atgacatccg | cttggccgac | 1380 |
| 374 | atggacctgc | ggttcagggt | cctcgagacc | gccagctaca | acgggggtgct | gatctggaag | 1440 |
| 376 | atccgtgact | acaagcgccg | gaagcaggag | gccgtcatgg | ggaagaccct | gtctctctac | 1500 |
| 378 | agccagcctt | tctacacagg | ttatttggc | tataagatgt | gtgccagggt | ctacctgaat | 1560 |
| 380 | ggggacggaa | tggggaaagg | gacacacttg | tcgctgtttt | ttgtcattat | gcgtggagaa | 1620 |
| 382 | tatgatgctc | tgttgcctatg | gccgttcaag | cagaaagtga | cacttatgtc | gatggatcag | 1680 |
| 384 | gggtcctctc | gccgtcatct | gggagatgctg | ttcaaggctg | accccaacag | cagcagcttc | 1740 |
| 386 | aagaaaaccc | ccggagagat | gaatatcgcc | tctggctgccc | cagtcttgc | cgcccaaact | 1800 |
| 388 | gttctagaga | acgggacgta | tattaaagat | gatacaatct | ttattaaggt | catagtggat | 1860 |
| 390 | acctcgatc | tgcctgaccc | ctgacaagaa | agcaggcgg | tggattcagc | agaaggtaac | 1920 |
| 392 | tcctctgggg | gggtgagcta | gtgtcttcac | ggaggtcctc | gccctcagaa | aggaccttgc | 1980 |
| 394 | ggcgcagagg | aagcagccgg | aggaggagaa | ggaggtcgag | tggctggcag | gagagccaca | 2040 |
| 396 | tgtaaaaaca | gaccccaacg | gattttctaa | taaactagcc | acacccactc | tgaaggattt | 2100 |
| 398 | tttatccatc | aacaagataa | atactgctgt | cagagaaggt | tttcattttc | attttaaaag | 2160 |
| 400 | atctagttt | aagggtggaa | catatatgt | aaaaagaaac | atgattttc | ttccttaact | 2220 |
| 402 | taaaacacca | aaagagaaca | catgtgggg | tagctgggt | gtgtacagta | cctcgaggc | 2280 |
| 404 | ttaaaatcat | aaacaatcac | atactcatcc | taaaattcag | ggtgcaactc | cgtttcaaata | 2340 |
| 406 | attgtatatt | gtctatttt | | | | | 2359 |
| 409 | <210> | SEQ ID NO: | 4 | | | | |
| 410 | <211> | LENGTH: | 2455 | | | | |
| 411 | <212> | TYPE: | DNA | | | | |
| 412 | <213> | ORGANISM: | Homo Sapiens | | | | |
| 414 | <400> | SEQUENCE: | 4 | | | | |
| 415 | ccccggggagcg | ccgcgcggcc | gccgcgtgcg | cgagccgggg | ttgcagccca | gccgggactt | 60 |
| 417 | tccagccggc | ggcagccggc | ggggcgtgcg | gctttcccc | gccccccgtc | atggggcagc | 120 |
| 419 | ccggggagca | gaacgctgcg | gaccgcggcg | gaggacgcgc | ccggcgcggcc | tgagccggcc | 180 |
| 421 | gagcggcgcac | ggaccgcgag | aactccttt | tcctaaaatg | gagtcgagta | aaaagatgg | 240 |
| 423 | ctctccctggc | gcccgtcaga | ctaaccgcgc | gtctaaagctg | cacactgacc | gtatgtctgg | 300 |
| 425 | gacgcctagg | tttgcctctg | aacaaggagg | ttacaaggaa | aagtttgc | agaccgtgg | 360 |
| 427 | ggacaagtac | aagtgtgaga | agtgcacact | ggtgctgtgc | agcccgaaac | agaccgagtg | 420 |
| 429 | tgggcaccgc | ttctgcgaga | gctgcgtgc | ggccctgtgc | agctcttcaa | gtccaaaatg | 480 |
| 431 | tacagcgtgt | caagagagca | tcgtttaaaa | taagtggtt | aaggataatt | gctgcaagag | 540 |
| 433 | agaaaattctg | gctcttcaga | tctattgtcg | gaatgaaagc | agagggtgt | cagacgttt | 600 |
| 435 | aacgctggga | catctgctgg | tgcatataaa | aaatgattgc | cattttgaag | aacttccatg | 660 |
| 437 | tgtgcgtcct | gactgaaag | aaaaggtctt | gagggaaagac | ctgcgagacc | acgtggagaa | 720 |
| 439 | ggcgtgtaaa | taccggaaag | ccacatcgac | ccactgcaag | agtcaagggtc | cgatgatgc | 780 |
| 441 | gctgcagaaa | cacgaagaca | ccgactgtcc | ctgcgtgggt | gtgtcctgccc | ctcacaagt | 840 |
| 443 | cagcgtccac | actctctga | ggagcgtgg | gagtcacac | ttgtcagatgt | gtgtcaatgc | 900 |
| 445 | ccccagcacc | tgtattttta | agcgtatgg | ctgcgtttt | caggggacaa | accacgt | 960 |
| 447 | caaggcccac | gaggccagct | ccgcccgtgc | gcacgtcaac | ctgctgaagg | agtggagcaa | 1020 |
| 449 | ctcgctcgaa | aagaaggttt | ccttgcgtgc | gaatgaaatgt | gtagaaaaaa | acaagagcat | 1080 |
| 451 | aaaaagtttgc | cacaatcaga | tatgtatgtt | tgttttttttt | atttttttttt | aaaaagggaaat | 1140 |
| 453 | gtttcgaaat | aatgaatcca | aaatccatca | tttacagcga | gtgtatcgaca | gccaagcaga | 1200 |
| 455 | aaaaactgaag | gagcttgaca | aggagatccg | gccctccgg | cagaactgggg | aggaagcaga | 1260 |
| 457 | cagcatgaag | agcagcgtgg | agtccctcca | gaaccgcgtg | accgagctgg | agagcgtgg | 1320 |
| 459 | caagagtgcg | gggcaagtgg | ctcggaaacac | aggcgtctgc | gagtcctcagc | tgagccggca | 1380 |
| 461 | tgaccagatg | ctgagtggtc | acgacatccg | cctagccgac | atggacctgc | gcttccaggt | 1440 |

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Wrong Format

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date